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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/082,894

DATE: 06/04/2002

TIME: 12:37:17

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\06042002\J082894.raw

ENTERED

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4 <110> APPLICANT: Kloek, Andrew P.
5     Williams, Deryck Jeremy
6     Salmon, Brandy Leigh
7     Bradley, John D.
9 <120> TITLE OF INVENTION: NEMATODE PGM-LIKE SEQUENCES
11 <130> FILE REFERENCE: 12557-003001
13 <140> CURRENT APPLICATION NUMBER: US 10/082,894
14 <141> CURRENT FILING DATE: 2002-02-26
16 <150> PRIOR APPLICATION NUMBER: US 60/271,781
17 <151> PRIOR FILING DATE: 2001-02-27
19 <160> NUMBER OF SEQ ID NOS: 14
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1719
25 <212> TYPE: DNA
26 <213> ORGANISM: Meloidogyne incognita PGM
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (22)...(1599)
32 <400> SEQUENCE: 1
33 gtttaattac ccaagtttga g atg gac aaa tat caa aat gtt caa caa aaa      51
34                               Met Asp Lys Tyr Gln Asn Val Gln Gln Lys
35                               1           5           10
37 gtc tgt ctt gta gtt att gat gga tgg ggc ctt tcc gat gaa caa cac      99
38 Val Cys Leu Val Val Ile Asp Gly Trp Gly Leu Ser Asp Glu Gln His
39                               15           20           25
41 ggg aat gca att gct aaa gct aaa acg cct att atg gac aaa ctt tgt      147
42 Gly Asn Ala Ile Ala Lys Ala Lys Thr Pro Ile Met Asp Lys Leu Cys
43                               30           35           40
45 tct gga aat tgg caa aaa ttg gaa gca cac ggt ctt cat gtt gga ttg      195
46 Ser Gly Asn Trp Gln Lys Leu Glu Ala His Gly Leu His Val Gly Leu
47                               45           50           55
49 cca gaa ggc tta atg gga aat tct gaa gtt gga cat ttg aat ata gga      243
50 Pro Glu Gly Leu Met Gly Asn Ser Glu Val Gly His Leu Asn Ile Gly
51                               60           65           70
53 gct gga aga gtt att tat caa gat att gtt cga att aat ttg gct gtt      291
54 Ala Gly Arg Val Ile Tyr Gln Asp Ile Val Arg Ile Asn Leu Ala Val
55 75           80           85           90
57 caa cga aac gag ttt gtt aca aat cct cag att gtt gca tca gct gag      339
58 Gln Arg Asn Glu Phe Val Thr Asn Pro Gln Ile Val Ala Ser Ala Glu
59                               95           100          105
61 cgt gca aag aag ggg agt ggt cga ttg cat tta tta gga ctg gtt agc      387
62 Arg Ala Lys Lys Gly Ser Gly Arg Leu His Leu Leu Gly Leu Val Ser

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63		110		115		120		
65	gat	ggt	ggt	gtc	cac	tct	cat	att
66	Asp	Gly	Gly	Val	His	Ser	His	Ile
67								
69	gca	ttt	aaa	caa	tta	caa	gtg	cca
70	Ala	Phe	Lys	Gln	Leu	Gln	Val	Pro
71								
73	gat	ggt	cga	gat	act	tcg	cca	aca
74	Asp	Gly	Arg	Asp	Thr	Ser	Pro	Thr
75	155							
77	ctt	ctt	caa	ttt	att	gct	tcg	gaa
78	Leu	Leu	Gln	Phe	Ile	Ala	Ser	Glu
79								
81	act	gga	cgt	tat	tat	gca	atg	gat
82	Thr	Gly	Arg	Tyr	Tyr	Ala	Met	Asp
83								
85	aag	atg	gct	tat	gag	gca	att	ggt
86	Lys	Met	Ala	Tyr	Glu	Ala	Ile	Val
87								
89	ggt	gat	aag	gct	gtc	gat	ggt	aga
90	Val	Asp	Lys	Ala	Val	Asp	Val	Arg
91								
93	act	gac	gaa	ttt	ctg	aaa	cca	att
94	Thr	Asp	Glu	Phe	Leu	Lys	Pro	Ile
95	235							
97	aaa	gat	gac	gat	act	ctt	att	ttc
98	Lys	Asp	Asp	Asp	Thr	Leu	Ile	Phe
99								
101	cgt	caa	att	tgt	gaa	tgt	ttg	ggt
102	Arg	Gln	Ile	Cys	Glu	Cys	Leu	Gly
103								
105	agt	tcg	ggt	cct	cac	cct	aaa	aat
106	Ser	Ser	Val	Pro	His	Pro	Lys	Asn
107								
109	tac	aat	aaa	gag	ttt	cca	ttt	cca
110	Tyr	Asn	Lys	Glu	Phe	Pro	Phe	Pro
111								
113	act	aat	gtg	ctt	gct	gaa	tggt	ctt
114	Thr	Asn	Val	Leu	Ala	Glu	Trp	Leu
115	315							
117	cac	tgt	gag	gaa	act	gag	aag	tat
118	His	Cys	Ala	Glu	Thr	Glu	Lys	Tyr
119								
121	ggt	ggt	cga	gaa	ggt	caa	ttc	caa
122	Gly	Gly	Arg	Glu	Val	Gln	Phe	Gln
123								
125	tca	cca	aaa	gaa	ggt	gct	aca	tat
126	Ser	Pro	Lys	Glu	Val	Ala	Thr	Tyr
127								

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129 gct gga gtt gcc gaa aaa atg gtc gag caa att gag tca ggc agg cat 1203
130 Ala Gly Val Ala Glu Lys Met Val Glu Gln Ile Glu Ser Gly Arg His
131 380 385 390
133 cct ttg gtt atg tgc aat ttt gcg cct cct gac atg gtt gga cat act 1251
134 Pro Leu Val Met Cys Asn Phe Ala Pro Pro Asp Met Val Gly His Thr
135 395 400 405 410
137 ggt aaa ttt gaa cct gcc gtc aaa gca tgt caa gct act gac gag gca 1299
138 Gly Lys Phe Glu Pro Ala Val Lys Ala Cys Gln Ala Thr Asp Glu Ala
139 415 420 425
141 att gga aag ata ttt gaa gca tgc caa act tat aat tac gtt ctt atg 1347
142 Ile Gly Lys Ile Phe Glu Ala Cys Gln Thr Tyr Asn Tyr Val Leu Met
143 430 435 440
145 gtt act tcc gat cat gga aat gct gag aag atg att gct ccc gat ggt 1395
146 Val Thr Ser Asp His Gly Asn Ala Glu Lys Met Ile Ala Pro Asp Gly
147 445 450 455
149 agt gaa cat act gca cat acc tgc aat ttg gtc cca ttt act tgc tct 1443
150 Ser Glu His Thr Ala His Thr Cys Asn Leu Val Pro Phe Thr Cys Ser
151 460 465 470
153 tcc aaa aca ttt gtt ttt aaa tcg act cca cct act gga gat gat ggc 1491
154 Ser Lys Thr Phe Val Phe Lys Ser Thr Pro Pro Thr Gly Asp Asp Gly
155 475 480 485 490
157 aaa gaa cgt gca cga gcc tta cgt gat gtt gca ccg act gtt cta caa 1539
158 Lys Glu Arg Ala Arg Ala Leu Arg Asp Val Ala Pro Thr Val Leu Gln
159 495 500 505
161 tta atg ggc tta cct gta ccg ccg gag atg gat ggc gtt cct tta ctt 1587
162 Leu Met Gly Leu Pro Val Pro Pro Glu Met Asp Gly Val Pro Leu Leu
163 510 515 520
165 gaa cag aga gga taagaagtta attgacaata ggaaataaat atgagctgct 1639
166 Glu Gln Arg Gly
167 525
169 attacaagca attttaaaaa ttttagtaaa acgagtaatt tttgatatat acatatttag 1699
170 aaatctccgt tataaaaatt 1719
172 <210> SEQ ID NO: 2
173 <211> LENGTH: 526
174 <212> TYPE: PRT
175 <213> ORGANISM: Meloidogyne incognita PGM
177 <400> SEQUENCE: 2
178 Met Asp Lys Tyr Gln Asn Val Gln Gln Lys Val Cys Leu Val Val Ile
179 1 5 10 15
180 Asp Gly Trp Gly Leu Ser Asp Glu Gln His Gly Asn Ala Ile Ala Lys
181 20 25 30
182 Ala Lys Thr Pro Ile Met Asp Lys Leu Cys Ser Gly Asn Trp Gln Lys
183 35 40 45
184 Leu Glu Ala His Gly Leu His Val Gly Leu Pro Glu Gly Leu Met Gly
185 50 55 60
186 Asn Ser Glu Val Gly His Leu Asn Ile Gly Ala Gly Arg Val Ile Tyr
187 65 70 75 80
188 Gln Asp Ile Val Arg Ile Asn Leu Ala Val Gln Arg Asn Glu Phe Val
189 85 90 95

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```

190 Thr Asn Pro Gln Ile Val Ala Ser Ala Glu Arg Ala Lys Lys Gly Ser
191          100          105          110
192 Gly Arg Leu His Leu Leu Gly Leu Val Ser Asp Gly Gly Val His Ser
193          115          120          125
194 His Ile Asp His Leu Phe Ala Leu Ile Arg Ala Phe Lys Gln Leu Gln
195          130          135          140
196 Val Pro Lys Val Phe Ile His Phe Phe Ala Asp Gly Arg Asp Thr Ser
197 145          150          155          160
198 Pro Thr Ser Gly Ala Gly Tyr Leu Glu Gln Leu Leu Gln Phe Ile Ala
199          165          170          175
200 Ser Glu Lys Tyr Gly Glu Leu Ala Thr Ile Thr Gly Arg Tyr Tyr Ala
201          180          185          190
202 Met Asp Arg Asp Lys Arg Trp Glu Arg Ile Lys Met Ala Tyr Glu Ala
203          195          200          205
204 Ile Val Gly Gly Ile Gly Gln Lys Ala Thr Val Asp Lys Ala Val Asp
205          210          215          220
206 Val Val Arg Glu Arg Tyr Ala Gln Ser Glu Thr Asp Glu Phe Leu Lys
207 225          230          235          240
208 Pro Ile Val Phe Ser Asp Asp Gly Arg Val Lys Asp Asp Asp Thr Leu
209          245          250          255
210 Ile Phe Phe Asn Tyr Arg Ala Asp Arg Met Arg Gln Ile Cys Glu Cys
211          260          265          270
212 Leu Gly Leu Glu Arg Tyr Lys Asp Leu Asn Ser Ser Val Pro His Pro
213          275          280          285
214 Lys Asn Ile Gln Ile Ser Gly Met Thr Gln Tyr Asn Lys Glu Phe Pro
215          290          295          300
216 Phe Pro Ser Leu Phe Pro Pro Val Thr His Thr Asn Val Leu Ala Glu
217 305          310          315          320
218 Trp Leu Ala Ser Gln Gly Val Thr Gln Phe His Cys Ala Glu Thr Glu
219          325          330          335
220 Lys Tyr Pro His Val Thr Phe Phe Phe Asn Gly Gly Arg Glu Val Gln
221          340          345          350
222 Phe Gln Asp Glu Glu Arg Cys Met Val Pro Ser Pro Lys Glu Val Ala
223          355          360          365
224 Thr Tyr Asp Leu Lys Pro Glu Met Asn Ala Ala Gly Val Ala Glu Lys
225          370          375          380
226 Met Val Glu Gln Ile Glu Ser Gly Arg His Pro Leu Val Met Cys Asn
227 385          390          395          400
228 Phe Ala Pro Pro Asp Met Val Gly His Thr Gly Lys Phe Glu Pro Ala
229          405          410          415
230 Val Lys Ala Cys Gln Ala Thr Asp Glu Ala Ile Gly Lys Ile Phe Glu
231          420          425          430
232 Ala Cys Gln Thr Tyr Asn Tyr Val Leu Met Val Thr Ser Asp His Gly
233          435          440          445
234 Asn Ala Glu Lys Met Ile Ala Pro Asp Gly Ser Glu His Thr Ala His
235          450          455          460
236 Thr Cys Asn Leu Val Pro Phe Thr Cys Ser Ser Lys Thr Phe Val Phe
237 465          470          475          480
238 Lys Ser Thr Pro Pro Thr Gly Asp Asp Gly Lys Glu Arg Ala Arg Ala

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239          485          490          495
240 Leu Arg Asp Val Ala Pro Thr Val Leu Gln Leu Met Gly Leu Pro Val
241          500          505          510
242 Pro Pro Glu Met Asp Gly Val Pro Leu Leu Glu Gln Arg Gly
243          515          520          525
245 <210> SEQ ID NO: 3
246 <211> LENGTH: 539
247 <212> TYPE: PRT
248 <213> ORGANISM: Caenorhabditis elegans PGM
250 <400> SEQUENCE: 3
251 Met Phe Val Ala Leu Gly Ala Gln Ile Tyr Arg Gln Tyr Phe Gly Arg
252   1          5          10          15
253 Arg Gly Met Ala Met Ala Asn Asn Ser Ser Val Ala Asn Lys Val Cys
254          20          25          30
255 Leu Ile Val Ile Asp Gly Trp Gly Val Ser Glu Asp Pro Tyr Gly Asn
256          35          40          45
257 Ala Ile Leu Asn Ala Gln Thr Pro Val Met Asp Lys Leu Cys Ser Gly
258          50          55          60
259 Asn Trp Ala Gln Ile Glu Ala His Gly Leu His Val Gly Leu Pro Glu
260  65          70          75          80
261 Gly Leu Met Gly Asn Ser Glu Val Gly His Leu Asn Ile Gly Ala Gly
262          85          90          95
263 Arg Val Ile Tyr Gln Asp Ile Val Arg Ile Asn Leu Ala Val Lys Asn
264          100         105         110
265 Asn Lys Phe Val Thr Asn Glu Ser Leu Val Asp Ala Cys Asp Arg Ala
266          115         120         125
267 Lys Asn Gly Asn Gly Arg Leu His Leu Ala Gly Leu Val Ser Asp Gly
268          130         135         140
269 Gly Val His Ser His Ile Asp His Met Phe Ala Leu Val Lys Ala Ile
270 145         150         155         160
271 Lys Glu Leu Gly Val Pro Glu Leu Tyr Leu His Phe Tyr Gly Asp Gly
272          165         170         175
273 Arg Asp Thr Ser Pro Asn Ser Gly Val Gly Phe Leu Glu Gln Thr Leu
274          180         185         190
275 Glu Phe Leu Glu Lys Thr Thr Gly Tyr Gly Lys Leu Ala Thr Val Val
276          195         200         205
277 Gly Arg Tyr Tyr Ala Met Asp Arg Asp Asn Arg Trp Glu Arg Ile Asn
278          210         215         220
279 Val Ala Tyr Glu Ala Met Ile Gly Gly Val Gly Glu Thr Ser Asp Glu
280 225         230         235         240
281 Ala Gly Val Val Glu Val Val Arg Lys Arg Tyr Ala Ala Asp Glu Thr
282          245         250         255
283 Asp Glu Phe Leu Lys Pro Ile Ile Leu Gln Gly Glu Lys Gly Arg Val
284          260         265         270
285 Gln Asn Asp Asp Thr Ile Ile Phe Phe Asp Tyr Arg Ala Asp Arg Met
286          275         280         285
287 Arg Glu Ile Ser Ala Ala Met Gly Met Asp Arg Tyr Lys Asp Cys Asn
288          290         295         300
289 Ser Lys Leu Ala His Pro Ser Asn Leu Gln Val Tyr Gly Met Thr Gln

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VERIFICATION SUMMARY

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Input Set : A:\SEQUENCE LISTING.txt

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